

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 219.37 Seconds
(without alignments)
4337.914 Million cell updates/sec

Title: US-09-943-115A-8

Perfect score: 25

Sequence: 1 tcttagagctcttcctccaccacaaact 25

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gsal.*

9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.8	87.2	810	6	CB339857 CA23EI02I
2	20.2	80.8	626	8	AZ307169 IM008M04
3	19.8	79.2	455	6	CB741675 AMGNNUC:S
4	19.8	79.2	673	8	BZ803457 PUFQ089TD
5	19.8	79.2	843	9	CG183873 PUHN32TD
6	19.4	77.6	556	8	CC062244 ugm001e0
7	19.4	77.6	987	5	BQ956803 AGENCOURT
8	19.2	76.8	941	7	CO020587 EST16680
9	18.8	75.2	518	8	AZ808593 2M0072N11
10	18.6	74.4	182	2	BE223371 KP75G06.Y
11	18.6	74.4	344	7	CO939972 UMC-pd45f
12	18.6	74.4	349	5	BX914384 BX914384
13	18.6	74.4	430	5	BX982094 BX982094
14	18.6	74.4	472	8	BH275616 CH230-701
15	18.6	74.4	531	2	AV971360 AV971360
16	18.6	74.4	543	1	AL588321 AL588321
17	18.6	74.4	545	2	AV983945 AV983945
18	18.6	74.4	549	4	BG710511 BGL1n.pk0
19	18.6	74.4	551	5	BW042006 BW042006
20	18.6	74.4	565	1	AJ398343 AJ398343
21	18.6	74.4	577	8	AZ958073 2M0225N09
22	18.6	74.4	604	4	BI065397 BGL1n.pk0
23	18.6	74.4	604	5	BW078263 BW078263
24	18.6	74.4	616	9	AG339252 Lotus cor

25 18.6 74.4 625 4 BI065075
26 18.6 74.4 641 5 BW043881
27 18.6 74.4 643 4 EG713114
28 18.6 74.4 652 7 CK76252
29 18.6 74.4 676 1 AA702791
30 18.6 74.4 686 5 BW448117
31 18.6 74.4 690 5 BW090595
32 18.6 74.4 698 5 BW077639
33 18.6 74.4 702 5 BW033237
34 18.6 74.4 730 5 BW429347
35 18.6 74.4 750 9 CL014894
36 18.6 74.4 759 6 CB991210
37 18.6 74.4 762 8 AQ747999
38 18.6 74.4 768 7 CO983347
39 18.6 74.4 775 6 CB990421
40 18.6 74.4 786 5 BX871836
41 18.6 74.4 805 9 CC595391
42 18.6 74.4 808 6 CA512261
43 18.6 74.4 815 6 CB991778
44 18.6 74.4 835 7 CN321869
45 18.6 74.4 837 7 CN331567

ALIGNMENTS

RESULT 1
CB339857

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CB339857 810 bp mRNA linear EST 14-MAR-2003
CA23EI02IVRB_G02 Cabernet Sauvignon Leaf - CA23EI Vitis vinifera
cDNA clone CA23EI02IVRB_G02 3', mRNA sequence.

CB339857

CB339857.1

GI:28959713

EST

Vitis vinifera

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; Vitaceae; Vitis.

1 (bases 1 to 810)

Goes da Silva, F., Lim, H., Iandolino, A., Baek, J., Leslie, A., Xu, J.,

Jones, K., Walker, M.A., and Cook, D.R.

Transcriptional responses of Vitis vinifera to infection by the

bacterial pathogen Xylella fastidiosa

Unpublished (2003)

Contact: Douglas Cook, PhD

CAES Genome Facility

UC Davis, Plant Pathology

One Shields Ave, Davis, CA 95616, USA

Tel: 530 754 6561

Fax: 530 754 6617

Email: droco@ucdavis.edu

Seq primer: GCCAACGATGCTGCTAG.

Location/Qualifiers

1..810

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="CA23EI02IVRB_G02"

/sex="Hermaphrodite"

/dev_stage="Mid-season leaf material, collected July 25,

2001."

/lab_host="DHSalpha"

/clone_lib="Cabernet Sauvignon Leaf - CA23EI"

/note="Organ: Leaf; Vector: pDNR; Site: Sfil; Site 2:

Sfil; CA23EI is a cDNA library of Cabernet Sauvignon

leaves. The leaves were collected on July 25, 2001, in

Napa Valley, California, and represent leaves in

mid-season development. These leaves were verified to be

infected with the bacterial pathogen, Xylella fastidiosa,

based on a diagnostic assay using PCR and Xylella-specific

primer pairs. The plants were asymptomatic at the time of

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 140.652 Seconds
(without alignments)
1103.355 Million cell updates/sec

Title: US-09-943-115A-8
Perfect score: 25
Sequence: 1 tcttagagctcttctcaccacaaact 25

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
27: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	10	US-09-943-115A-8
C 2	25	100.0	1345	10	US-09-943-115A-1
C 3	25	100.0	1345	14	US-10-146-575-3
C 4	25	100.0	1345	14	US-10-085-612-3
C 5	25	100.0	12983	21	US-10-415-607-1
C 6	25	100.0	13035	15	US-10-121-960C-14
C 7	25	100.0	15185	15	US-10-121-960C-17
					Sequence 8, Appli
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 14, Appli
					Sequence 17, Appli

C 8	25	100.0	96960	21	US-10-484-577-662	Sequence 662, App
C 9	22.4	89.6	1012	9	US-09-957-997-4	Sequence 4, Appli
C 10	22.4	89.6	1186	9	US-09-957-997-1	Sequence 1, Appli
C 11	22.4	89.6	1186	21	US-10-415-607-4	Sequence 4, Appli
C 12	19.2	76.8	8943	17	US-10-257-166-47	Sequence 47, Appli
C 13	18.8	75.2	8205	9	US-09-860-670-276	Sequence 276, App
C 14	18.8	75.2	8205	17	US-10-227-646-276	Sequence 276, App
C 15	18.8	75.2	2666	13	US-10-087-192-1777	Sequence 1777, App
C 16	18.8	75.2	28446	19	US-10-331-053-13	Sequence 13, Appli
C 17	18.8	75.2	100685	19	US-10-388-838-93	Sequence 93, Appli
C 18	18.6	74.4	541	13	US-10-027-632-91527	Sequence 91527, A
C 19	18.6	74.4	541	13	US-10-027-632-307501	Sequence 307501, A
C 20	18.6	74.4	541	17	US-10-027-632-91527	Sequence 91527, A
C 21	18.6	74.4	541	17	US-10-027-632-307501	Sequence 307501, A
C 22	18.6	74.4	1254	14	US-10-085-612-4	Sequence 4, Appli
C 23	18.4	73.6	1223137	13	US-10-027-632-179264	Sequence 179264, A
C 24	18.4	73.6	1223137	17	US-10-027-632-179264	Sequence 179264, A
C 25	18.2	72.8	508	9	US-09-878-178-2224	Sequence 2224, App
C 26	18.2	72.8	508	13	US-10-046-935-2224	Sequence 2224, App
C 27	18.2	72.8	508	14	US-10-146-502-2224	Sequence 2224, App
C 28	18.2	72.8	589	21	US-10-487-901-1682	Sequence 1682, App
C 29	18.2	72.8	633	13	US-10-027-632-255622	Sequence 255622, A
C 30	18.2	72.8	633	17	US-10-027-632-255622	Sequence 255622, A
C 31	18.2	72.8	637	13	US-10-027-632-188102	Sequence 188102, A
C 32	18.2	72.8	637	17	US-10-027-632-188102	Sequence 188102, A
C 33	18.2	72.8	4145	20	US-10-335-053-230	Sequence 230, App
C 34	18.2	72.8	104729	20	US-10-723-860-1434	Sequence 1434, App
C 35	17.8	71.2	559	13	US-10-027-632-231930	Sequence 231930, A
C 36	17.6	70.4	337	21	US-10-027-632-231930	Sequence 231930, A
C 37	17.6	70.4	337	21	US-10-914-037-898	Sequence 898, App
C 38	17.6	70.4	437	9	US-09-878-178-1397	Sequence 1397, App
C 39	17.6	70.4	437	13	US-10-046-935-1397	Sequence 1397, App
C 40	17.6	70.4	437	14	US-10-146-503-1397	Sequence 1397, App
C 41	17.6	70.4	558	19	US-10-437-963-200	Sequence 200, App
C 42	17.6	70.4	685	13	US-10-027-632-199874	Sequence 199874, A
C 43	17.6	70.4	685	17	US-10-027-632-199874	Sequence 199874, A
C 44	17.6	70.4	1086	10	US-09-814-353-19227	Sequence 19227, A
C 45	17.6	70.4	1391	9	US-09-969-708-480	Sequence 480, App

ALIGNMENTS

RESULT 1
US-09-943-115A-8
; Sequence 8, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943,115A
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-943-115A-8

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:12:33 ; Search time 24.8229 Seconds
(without alignments)
5961.965 Million cell updates/sec

Title: US-09-943-115a-8

Perfect score: 25

Sequence: 1 tcttagagctcttctcaccacaaact 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001s:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2002bs:*

8: Geneseqn2003s:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	6	ABK68752 PCR prime
C 2	25	100.0	1345	2	AAX28296 Human CYP
C 3	25	100.0	1345	3	AAX57019 Nucleic a
C 4	25	100.0	1345	3	AAX57020 Nucleic a
C 5	25	100.0	1345	6	ABK68745 5'-flanki
C 6	25	100.0	1345	12	ADJ84441 Human phe
C 7	25	100.0	6101	13	ADJ84441 Human CYP
C 8	25	100.0	12983	6	ADJ84441 Human CYP
C 9	25	100.0	13035	8	AAD41239 Human CYP
C 10	25	100.0	15185	8	AAD51897 Human CYP
C 11	25	100.0	39071	12	ADM97420 Prostate
C 12	25	100.0	96960	8	ACF62734 Cancer ba
C 13	25	100.0	96960	8	ADB20849 MRPI base
C 14	25	100.0	96960	10	ADB87938 Human UGT
C 15	25	100.0	96960	10	ADB87938 Human UGT
C 16	25	100.0	96960	10	ADB87938 Human UGT
C 17	25	100.0	123785	10	ABX77171 DNA seque
C 18	22.4	89.6	1012	6	AAD36215 Human pro
C 19	22.4	89.6	11186	6	AAD41242 Human CYP
C 20	22.4	89.6	11186	6	AAD36213 Human cyt

C 21	21.8	87.2	6101	13	ADS89689	Ad89689 Oligonucle
C 22	21.8	87.2	6101	13	ADS89415	Ad89415 Oligonucle
C 23	19.2	76.8	8943	6	ABK39966	Abk39966 Human che
C 24	18.8	75.2	8205	4	AAK90749	Aak90749 Human dig
C 25	18.8	75.2	8205	4	AAI62948	Aai62948 Human gen
C 26	18.8	75.2	26666	11	ACN45032	Acn45032 Mouse gen
C 27	18.8	75.2	100685	13	ABD32735	Abd32735 Mouse can
C 28	18.6	74.4	830	6	ABK99410	Abk99410 Human CYP
C 29	18.6	74.4	830	6	ABK99524	Abk99524 Human CYP
C 30	18.6	74.4	830	6	ABK99501	Abk99501 Human CYP
C 31	18.6	74.4	830	6	ABK99411	Abk99411 Human CYP
C 32	18.6	74.4	830	6	ABK99409	Abk99409 Human CYP
C 33	18.6	74.4	830	6	ABK99499	Abk99499 Human CYP
C 34	18.6	74.4	830	6	ABK99500	Abk99500 Human CYP
C 35	18.6	74.4	830	6	ABK99412	Abk99412 Human CYP
C 36	18.6	74.4	1346	3	AAA51756	Aaa51756 Cytochrom
C 37	18.6	74.4	2100	13	ADR07385	Adr07385 Full leng
C 38	18.2	72.8	511	6	ABL38635	Ab138635 Human col
C 39	18.2	72.8	589	10	ADK54299	Adk54299 Plant DNA
C 40	18.2	72.8	1434	10	ADD17894	Ad17894 DNA (Seqi
C 41	18.2	72.8	2233	10	ADF16076	Adf16076 Human alb
C 42	18.2	72.8	4145	10	ADD29781	Add29781 Human tum
C 43	18.2	72.8	104729	12	ADQ18615	Adq18615 Human eof
C 44	17.6	70.4	500	6	ABL37808	Ab137808 Human col
C 45	17.6	70.4	608	6	ABN62332	Abn62332 Human can

ALIGNMENTS

RESULT 1

ABK68752

ID ABK68752 standard; DNA; 25 BP.

AC ABK68752;

DT 02-JUL-2002 (first entry)

DE PCR primer #2 for detecting SNP in 5'-region of human CYP3A4 gene.

Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4; PCR; primer; ss.

OS Homo sapiens.

XX WO200218641-A2.

XX 07-MAR-2002.

PF 30-AUG-2001; 2001WO-IB001580.

XX 30-AUG-2000; 2000GB-00021286.

XX (GEMI-) GEMINI GENOMICS PLC.

PI Risinger C, Andersson MK, Lewander T, Olaisson E;

DR WPI; 2002-351712/38.

Novel primer pairs and sequence determination oligonucleotides useful for amplifying and detecting novel single nucleotide polymorphisms in the 5' flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes respectively.

Claim 2; Page 15; 47pp; English.

The present invention relates to PCR primer pairs for amplifying and sequence determination oligonucleotides for detecting single nucleotide polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450 (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position 461 of a defined 1345 base pair sequence for CYP3A4 or position 957, 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9. The PCR primers are useful for amplifying the CYP sequences and the

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OM nucleic - nucleic search, using sw model

Run On: June 19, 2005, 15:18:28 ; Search time 127.727 Seconds
(without alignments)
9484.165 Million cell updates/sec

Title: US-09-943-115A-8

Perfect score: 25
Sequence: 1 tcttagagttcttctcaccacaaact 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	25	100.0	25	6	AX421260	AX421260 Sequence
C 2	25	100.0	1013	9	AF181105	AF181105 Homo sapi
C 3	25	100.0	1345	6	AR142139	AR142139 Sequence
C 4	25	100.0	1345	6	AR142140	AR142140 Sequence
C 5	25	100.0	1345	6	BD222974	BD222974 CYP3A4 NF
C 6	25	100.0	1345	6	BD222975	BD222975 CYP3A4 NF
C 7	25	100.0	1345	6	CQ776018	CQ776018 Sequence
C 8	25	100.0	1345	6	CQ790615	CQ790615 Sequence
C 9	25	100.0	1345	6	AR222893	AR222893 Sequence
C 10	25	100.0	1345	6	AX421253	AX421253 Sequence
C 11	25	100.0	1345	9	HUMCYP3A4	D11131 Homo sapien
C 12	25	100.0	6101	6	CQ806643	CQ806643 Sequence
C 13	25	100.0	11374	9	AF185589	AF185589 Homo sapi
C 14	25	100.0	96960	6	AX706964	AX706964 Sequence
C 15	25	100.0	96960	6	AX707894	AX707894 Sequence
C 16	25	100.0	123778	9	AC069294	AC069294 Homo sapi
C 17	25	100.0	170470	9	AC146392	AC146392 Pan trogl
C 18	25	100.0	174832	9	AF280107	AF280107 Homo sapi
C 19	23.4	93.6	173861	2	AC141417	AC141417 Papio anu

C 20	23.4	93.6	183854	2	AC145951	AC145951 Pan trogl
C 21	22.4	89.6	1012	9	AF181861	AF181861 Homo sapi
C 22	22.4	89.6	11186	9	AF329900	AF329900 Homo sapi
C 23	21.8	87.2	6101	6	CQ806981	CQ806981 Sequence
C 24	21.8	87.2	6101	6	CQ807255	CQ807255 Sequence
C 25	20.4	81.6	190317	2	AC137848	AC137848 Mus muscu
C 26	20.2	80.8	121130	2	AC151659	AC151659 Dasyypu n
C 27	20.2	80.8	143723	2	AC101763	AC101763 Mus muscu
C 28	20.2	80.8	235733	2	AC114859	AC114859 Rattus no
C 29	20.2	80.8	235739	2	AC121421	AC121421 Rattus no
C 30	19.8	79.2	42566	2	AC149313	AC149313 Phakophor
C 31	19.8	79.2	165235	10	AC145398	AC145398 Rattus no
C 32	19.8	79.2	192707	2	AC116250	AC116250 Rattus no
C 33	19.8	79.2	195798	2	AC118890	AC118890 Rattus no
C 34	19.8	79.2	252721	2	AC095946	AC095946 Rattus no
C 35	19.4	77.6	110000	2	AC073157	AC073157 Homo sapi
C 36	19.4	77.6	115984	9	HS292F10	HS292F10 Human DNA
C 37	19.4	77.6	120664	9	AP000887	AP000887 Homo sapi
C 38	19.4	77.6	163999	2	AC141207	AC141207 Rattus no
C 39	19.4	77.6	167398	9	AC069227	AC069227 Homo sapi
C 40	19.4	77.6	171266	9	AF404777	AF404777 Homo sapi
C 41	19.4	77.6	226406	2	AC095975	AC095975 Rattus no
C 42	19.4	77.6	234457	2	AC109698	AC109698 Rattus no
C 43	19.4	77.6	234597	2	AC127638	AC127638 Rattus no
C 44	19.4	77.6	257605	2	AC120627	AC120627 Rattus no
C 45	19.4	77.6	267829	2	AC120979	AC120979 Rattus no

ALIGNMENTS

RESULT 1
AX421260
LOCUS AX421260 25 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 8 from Patent WO0218641.
ACCESSION AX421260
VERSION AX421260.1 GI:21524668
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Risinger, C., Andersson, M.K., Lewander, T. and Olaisson, E.
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms
JOURNAL Patent: WO 0218641-A 8 07-MAR-2002;
FEATURES
Gemini Genomics PLC (GB)
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTTAGAGTCTTCTCTCACCACAACT 25
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Db 1 TCTTAGAGTCTTCTCTCACCACAACT 25

RESULT 2
AF181105/c
LOCUS AF181105 1013 bp DNA linear PRI 10-SEP-1999
DEFINITION Homo sapiens cytochrome P-45011A4 (CYP3A4) gene, promoter region.
ACCESSION AF181105
VERSION AF181105.1 GI:5853303
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 175.496 Seconds
(without alignments)
4337.914 Million cell updates/sec

Title: us-09-943-115a-7

Perfect score: 20
Sequence: 1 ccagcctgaagtcagaga 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	19	95.0	553	4	BG039424 NXSI_098
5	19	95.0	565	6	CD923330 G750.107N
6	19	95.0	636	7	CD936872 OV.105F13
7	17.4	87.0	203	7	CV330241 IL2-UT007
8	17.4	87.0	325	2	BE776859 MY-21-E-0
9	17.4	87.0	346	9	CE095752 tigr-gss
10	17.4	87.0	404	1	AA729069 mw03a09.s
11	17.4	87.0	409	5	BA482078 DKFZp686N
12	17.4	87.0	569	5	BA920785 BX920785
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16	17.4	87.0	631	9	CE703536 tigr-gss
17	17.4	87.0	652	1	AI445869 t1j2g12.x
18	17.4	87.0	729	6	CA345627 676319 NC
19	17.4	87.0	749	6	CA348148 679395 NC
20	17	85.0	437	4	BJ682390 BJ682390
21	17	85.0	443	4	BI063793 IL3-UT011
22	17	85.0	461	7	CV419454 RC4-C1019
23	17	85.0	476	4	BI397594 NXPV 101
24	17	85.0	498	4	BG832753 NXPV_079_

25	17	85.0	615	1	AJ737738
26	17	85.0	665	5	BU212860 604153436
27	17	85.0	691	4	BJ685677 BJ685677
28	17	85.0	694	4	BJ676309 BJ676309
29	17	85.0	696	1	AJ737746
30	17	85.0	794	5	BU239104 603323633
31	17	85.0	818	5	BU226227 603948862
32	17	85.0	833	5	BU248598 603591241
33	16.8	84.0	228	2	BB227240 BB227240
34	16.8	84.0	344	4	BI317060 saf84c02
35	16.8	84.0	349	8	BZ848825 CH240_240
36	16.8	84.0	403	6	CB812370 AMGNNUC:S
37	16.8	84.0	430	4	BI941950 se11109.Y
38	16.8	84.0	434	4	BG306587 fm16b01.Y
39	16.8	84.0	462	1	AA645349 v87905.Y
40	16.8	84.0	476	1	AI592418 v87905.Y
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45	16.8	84.0	515	8	AQ970303 RFCl-23-3

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION wrel.pk0002.a5 wrel Triticum aestivum cDNA clone wrel.pk0002.a5 5'
end, mRNA sequence.
ACCESSION CA637269
VERSION CA637269.1 GI:25215565
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 511)
Tingey.S.V., Powell.W., Wolters.P., Dolan.M., Hainey.C., Yuan.Z.,
Miao.G., Caraher.N. and Hanafey.M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
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XhoI; Wheat (Triticum aestivum L.) root; 7 day old
etiolated seedling"

Query Match 95.0%; Score 19; DB 6; Length 511;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCAGCCTGAAGTCAGAG 19
Db 82 CCAGCCTGAAGTCAGAG 100

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 112.521 Seconds
(without alignments)
1103.355 Million cell updates/sec

Title: US-09-943-115A-7

Perfect score: 20

Sequence: 1 ccagcctgaagtgcagaga 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	20	100.0	12983	21	US-10-415-607-1
6	20	100.0	13035	15	US-10-121-960C-14
7	20	100.0	15185	15	US-10-121-960C-17

8	20	100.0	96960	21	US-10-484-577-662	Sequence 662, App
9	19	95.0	533	13	US-10-027-632-239621	Sequence 239621,
10	19	95.0	533	17	US-10-027-632-239621	Sequence 239621,
11	17.4	87.0	478	10	US-09-918-995-20604	Sequence 20604, A
12	17	85.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
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17	16.8	84.0	734	13	US-10-027-632-139509	Sequence 139509,
18	16.8	84.0	734	17	US-10-027-632-139509	Sequence 139509,
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20	16.8	84.0	800	17	US-10-027-632-139510	Sequence 139510,
21	16.8	84.0	905	19	US-10-437-963-8166	Sequence 8166, Ap
22	16.8	84.0	1031	18	US-10-425-114-7314	Sequence 7314, Ap
23	16.8	84.0	1090	13	US-10-027-632-30396	Sequence 30396, A
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25	16.8	84.0	1341	18	US-10-424-599-100092	Sequence 100092,
26	16.8	84.0	2194	18	US-10-424-599-83842	Sequence 83842, A
27	16.8	84.0	3177	9	US-09-801-574-3	Sequence 3, Appli
28	16.8	84.0	90541	9	US-09-759-359A-3	Sequence 3, Appli
29	16.8	84.0	90541	16	US-10-207-973-3	Sequence 3, Appli
30	16.8	84.0	90541	19	US-10-799-676-3	Sequence 3, Appli
31	16.8	84.0	219352	19	US-10-322-281-45	Sequence 45, Appli
32	16.8	84.0	220224	13	US-10-087-192-1282	Sequence 1282, Ap
33	16.4	82.0	354	13	US-10-027-632-268083	Sequence 268083,
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38	16.4	82.0	578	19	US-10-021-323-1108	Sequence 1108, Ap
39	16.4	82.0	870	9	US-09-738-626-766	Sequence 766, App
40	16.4	82.0	1425	17	US-10-282-122A-41529	Sequence 41529, A
41	16.4	82.0	1489	21	US-10-764-420-2629	Sequence 2629, Ap
42	16.4	82.0	114693	20	US-10-473-392-3	Sequence 3, Appli
43	16.4	82.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
44	16	80.0	428	13	US-10-027-632-60248	Sequence 60248, A
45	16	80.0	428	17	US-10-027-632-60248	Sequence 60248, A

ALIGNMENTS

RESULT 1
US-09-943-115A-7
Sequence 7, Application US/09943115A
Publication No. US20030017469A1
GENERAL INFORMATION:
APPLICANT: SEQUENOM, Inc.
APPLICANT: Risinger, Carl
APPLICANT: Andersson, Maria
APPLICANT: Lewander, Tommy
APPLICANT: Olafsson, Erik
TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
TITLE OF INVENTION: POLYMORPHISMS
FILE REFERENCE: 52459-20021.00
CURRENT APPLICATION NUMBER: US/09/943,115A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UK 0021286.0
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-943-115A-7

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 19:46:29 ; Search time 5.73654 Seconds
(without alignments)
5704.747 Million cell updates/sec

Title: US-09-943-115A-7

Perfect score: 20
Sequence: 1 ccagcctgaagtgcagaga 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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5: /cgm2_6/ptodata/1/ina/PTCUT COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	1345	US-09-144-367-3	Sequence 3, Appli
4	20	100.0	31197	US-09-949-016-12963	Sequence 12963, A
5	20	100.0	103934	US-09-949-016-14333	Sequence 14333, A
C 6	17.4	87.0	63658	US-09-949-016-13238	Sequence 13238, A
C 7	17.4	87.0	64489	US-09-949-016-11766	Sequence 11766, A
8	17.4	87.0	144158	US-09-949-016-11755	Sequence 11755, A
9	17.4	87.0	144158	US-09-949-016-12936	Sequence 12936, A
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12	16.8	84.0	601	US-09-949-016-197923	Sequence 197923, A
C 13	16.8	84.0	56616	US-09-949-016-12462	Sequence 12462, A
C 14	16.8	84.0	56616	US-09-949-016-17085	Sequence 17085, A
C 15	16.8	84.0	90541	US-09-759-359A-3	Sequence 3, Appli
C 16	16.8	84.0	90541	US-10-207-973-3	Sequence 3, Appli
C 17	16.8	84.0	156651	US-09-949-016-17349	Sequence 17349, A
C 18	16.4	82.0	990	US-09-603-208A-71	Sequence 71, Appl
C 19	15.8	79.0	156	US-09-621-976-11838	Sequence 11838, A
C 20	15.8	79.0	601	US-09-949-016-161246	Sequence 161246, A
C 21	15.8	79.0	601	US-09-949-016-175645	Sequence 175645, A
C 22	15.8	79.0	848	US-09-221-017B-443	Sequence 443, Appl
C 23	15.8	79.0	1132	US-08-651-136C-21	Sequence 21, Appl
C 24	15.8	79.0	1132	US-09-229-911A-21	Sequence 21, Appl
C 25	15.8	79.0	5688	US-09-949-016-16734	Sequence 16734, A
C 26	15.8	79.0	11002	US-09-949-016-17471	Sequence 17471, A
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C 29	15.8	79.0	20721	4	US-09-949-016-16257	Sequence 16257, A
C 30	15.8	79.0	31078	4	US-09-949-016-14435	Sequence 14435, A
C 31	15.8	79.0	44479	4	US-09-949-016-17176	Sequence 17176, A
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33	15.4	77.0	601	4	US-09-949-016-175699	Sequence 175699, A
34	15.4	77.0	601	4	US-09-949-016-198633	Sequence 198633, A
35	15.4	77.0	601	4	US-09-949-016-198634	Sequence 198634, A
36	15.4	77.0	1964	3	US-09-434-613-2	Sequence 2, Appli
37	15.4	77.0	1964	4	US-09-963-908-2	Sequence 2, Appli
38	15.4	77.0	1985	4	US-09-620-312D-812	Sequence 812, App
C 39	15.4	77.0	7584	4	US-09-949-016-11836	Sequence 11836, A
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C 41	15.4	77.0	767677	4	US-09-949-016-12147	Sequence 12147, A
C 42	15.4	77.0	767677	4	US-09-949-016-17361	Sequence 17361, A
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44	15.2	76.0	472	4	US-09-621-976-1189	Sequence 1189, Ap
45	15.2	76.0	548	4	US-09-702-705-1120	Sequence 1120, Ap

ALIGNMENTS

RESULT 1
US-09-372-339-1
; Sequence 1, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebbeck, Timothy
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-1

Query Match 100.0%; Score 20; DB 3; Length 1345;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 294 CCAGCCTGAAGTGCAGAGA 313

RESULT 2
US-09-372-339-2
; Sequence 2, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebbeck, Timothy
; APPLICANT: Felix, Carolyn
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-2

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:18:28 ; Search time 102.181 Seconds
(without alignments)
9484.165 Million cell updates/sec

Title: US-09-943-115A-7
Perfect score: 20
Sequence: 1 ccagcctgaaagtcagaga 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX421259
2	20	100.0	1001	6	CQ853861 Sequence
3	20	100.0	1013	9	AF181105 Homo sapi
4	20	100.0	1345	6	AR142139 Sequence
5	20	100.0	1345	6	AR142140 Sequence
6	20	100.0	1345	6	BD222974 CYP3A4 NF
7	20	100.0	1345	6	BD222975 CYP3A4 NF
8	20	100.0	1345	6	CQ776018 Sequence
9	20	100.0	1345	6	CQ790615 Sequence
10	20	100.0	1345	6	AR222893 Sequence
11	20	100.0	1345	6	AX421253 Sequence
12	20	100.0	1345	9	HUMCYP3A4
13	20	100.0	6101	6	CQ806643
14	20	100.0	11374	9	AF185589 Homo sapi
15	20	100.0	96960	6	AX706964 Sequence
16	20	100.0	96960	6	AX707894 Sequence
17	20	100.0	123778	9	AC069294 Homo sapi
18	20	100.0	174832	9	AF280107 Homo sapi
19	19	95.0	79355	2	AC021280 Homo sapi

C	20	19	95.0	155536	2	AC138877	AC138877 Homo sapi
	21	19	95.0	159287	9	AP003694	AP003694 Homo sapi
	22	19	95.0	161474	2	AC013697	AC013697 Homo sapi
C	23	19	95.0	175125	9	AC027031	AC027031 Homo sapi
C	24	19	95.0	190910	9	CNS01DUX	AL133372 Human chr
C	25	18.4	92.0	170470	9	AC146392	AC146392 Pan trogl
C	26	18.4	92.0	173861	2	AC141417	AC141417 Papio anu
C	27	18.4	92.0	208452	10	AC127291	AC127291 Mus muscu
C	28	18.4	92.0	222506	2	AC120726	AC120726 Rattus no
C	29	18.4	92.0	230518	2	AC097416	AC097416 Rattus no
C	30	18.4	92.0	231356	2	AC113626	AC113626 Rattus no
C	31	18	90.0	198857	9	AC012404	AC012404 Homo sapi
C	32	18	90.0	213865	2	AC145972	AC145972 Gallus ga
C	33	17.4	87.0	30175	9	AC004778	AC004778 Homo sapi
C	34	17.4	87.0	65937	2	AC102820	AC102820 Mus muscu
C	35	17.4	87.0	94000	9	AP000562	AP000562 Homo sapi
C	36	17.4	87.0	120173	9	AC137630	AC137630 Homo sapi
C	37	17.4	87.0	140300	9	AC015550	AC015550 Homo sapi
C	38	17.4	87.0	140739	9	AP005432	AP005432 Homo sapi
C	39	17.4	87.0	147731	8	AP005112	AP005112 Oryza sat
C	40	17.4	87.0	148508	2	AC027795	AC027795 Homo sapi
C	41	17.4	87.0	160215	10	AC092531	AC092531 Rattus no
C	42	17.4	87.0	163026	2	AC103883	AC103883 Homo sapi
C	43	17.4	87.0	163077	9	AC026362	AC026362 Homo sapi
C	44	17.4	87.0	163237	10	AC109192	AC109192 Mus muscu
C	45	17.4	87.0	166125	2	AC019327	AC019327 Homo sapi

ALIGNMENTS

RESULT 1
AX421259
LOCUS AX421259
DEFINITION Sequence 7 from Patent WO0218641.
ACCESSION AX421259
VERSION AX421259.1 GI:21524667
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Andersson,M&K., Lewander,T. and Olaisson,B.
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms
JOURNAL Patent: WO 0218641-A 7 07-MAR-2002;
GEMINI Genomics PLC (GB)
FEATURES
Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGCCTGAAAGTCAGAGA 20
DB 1 CCAGCCTGAAAGTCAGAGA 20
RESULT 2
CQ853861/c
LOCUS CQ853861 1001 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 121 from Patent WO2004067774.
ACCESSION CQ853861
VERSION CQ853861.1 GI:51509920
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:12:33; Search time 19.8584 Seconds
(without alignments)
5961.965 Million cell updates/sec

Title: US-09-943-115A-7

Perfect score: 20
Sequence: 1 ccagcctgaaagtcagaga 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1980s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2000s:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	Abk68751 PCR prime
2	20	100.0	201	12	Adm97390 Prostate
3	20	100.0	1001	13	Adq81033 Human phe
4	20	100.0	1345	2	Aax28296 Human CYP
5	20	100.0	1345	3	Aaz57019 Nucleic a
6	20	100.0	1345	3	Aaz57020 Nucleic a
7	20	100.0	1345	6	Abk68745 5'-flanki
8	20	100.0	1345	12	Adj84441 Human phe
9	20	100.0	6101	13	AdS89077 Human CYP
10	20	100.0	12983	6	Aad41239 Human CYP
11	20	100.0	13035	8	Aad51997 Human CYP
12	20	100.0	15185	8	Aad52000 Human CYP
13	20	100.0	39071	12	Adm97420 Prostate
14	20	100.0	96960	8	AcF62734 Cancer ba
15	20	100.0	96960	8	AdB20849 MRPI base
16	20	100.0	96960	10	AdB87938 Human UGT
17	20	100.0	96960	10	AdB96921 Human MDR
18	20	100.0	96960	10	AdB92112 Human MDR
19	20	100.0	123785	10	Abx77171 DNA sequ
20	17.4	87.0	478	9	ACH33392 Human end

c	21	17.4	87.0	57502	12	ADQ97092	Adg97092 Human can
c	22	17	85.0	349980	5	AAH68527	Aah68527 C Glutami
c	23	16.8	84.0	3177	5	AAH13624	Aah13624 CDNA sequ
c	24	16.8	84.0	90541	6	AB552847	Ab552847 Human SR
c	25	16.8	84.0	90541	10	ADJ37690	Adj37690 Human kin
c	26	16.8	84.0	90541	13	ADR31219	Adr31219 Human SRP
c	27	16.8	84.0	113033	8	AAH54213	Aah54213 SR protei
c	28	16.8	84.0	219352	13	ABD33098	Abd33098 Murine ca
c	29	16.8	84.0	220224	11	ACN44702	Acn44702 Human gen
c	30	16.4	82.0	419	3	ADP56956	Adp56956 Urogenita
c	31	16.4	82.0	578	13	ACN46327	Acn46327 Cotton pr
c	32	16.4	82.0	870	5	AAH65731	Aah65731 C Glutami
c	33	16.4	82.0	990	4	AAH71019	Aah71019 C. glutam
c	34	16.4	82.0	1425	8	ACA53659	Ac53659 Prokaryot
c	35	16.4	82.0	114693	8	AAD48308	Ad48308 Human tra
c	36	16.4	82.0	118384	10	ABX56555	Abx56555 Human aut
c	37	16.4	82.0	349980	5	AAH68526	Aah68526 C glutami
c	38	15.8	79.0	65	6	ABN30407	Abn30407 Rat splic
c	39	15.8	79.0	233	6	ABL84451	AbL84451 Human ova
c	40	15.8	79.0	305	2	AAV87197	Aav87197 EST clone
c	41	15.8	79.0	308	4	ABA71670	AbA71670 Human foe
c	42	15.8	79.0	308	4	AAI51966	Aai51966 Probe #20
c	43	15.8	79.0	308	4	AAK46056	Aak46056 Human bon
c	44	15.8	79.0	308	4	AAK20014	Aak20014 Human bra
c	45	15.8	79.0	308	4	ABS45762	AbS45762 Human liv

ALIGNMENTS

RESULT 1

ABK68751

ID ABK68751 standard; DNA; 20 BP.

XX

AC ABK68751;

XX

DT 02-JUL-2002 (first entry)

XX

DE PCR primer #1 for detecting SNP in 5'-region of human CYP3A4 gene.

XX

KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;

XX PCR; primer; ss.

XX Homo sapiens.

XX

PN WO200218641-A2.

XX

PD 07-MAR-2002.

XX

PF 30-AUG-2001; 2001WO-IB001580.

XX

PR 30-AUG-2000; 2000GB-00021286.

XX

PA (GEMI-) GEMINI GENOMICS PLC.

XX

PI Risinger C, Andersson MK, Lewander T, Olaisson B;

XX

DR WPI, 2002-351712/38.

XX

PT Novel primer pairs and sequence determination oligonucleotides useful for amplifying and detecting novel single nucleotide polymorphisms in the 5' flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes respectively.

XX

PS Claim 2; Page 15; 47pp; English.

XX

CC The present invention relates to PCR primer pairs for amplifying and sequence determination oligonucleotides for detecting single nucleotide polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450 (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position 461 of a defined 1345 base pair sequence for CYP3A4 or position 957, 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9. The PCR primers are useful for amplifying the CYP sequences and the

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 96.5227 Seconds
(without alignments)
4337.914 Million cell updates/sec

Title: US-09-943-115A-15

Perfect score: 11

Sequence: 1 gtgtgtacagc 11

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST:

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	67	CN869358	001202AAO
2	11	100.0	70	AI379030	tc53f01.x
3	11	100.0	70	AZ875009	AZ875009 2M0189A19
4	11	100.0	71	AZ936554	AZ936554 2M0193K13
5	11	100.0	85	CR181730	Reverse s
6	11	100.0	93	CR440674	CR440674 CR440674
7	11	100.0	100	CB395011	OSTR147F2
8	11	100.0	103	CV364386	PW1-GN030
9	11	100.0	104	BI017585	PM3-ET027
10	11	100.0	106	CR058606	Reverse s
11	11	100.0	108	BF334323	RC3-CT025
12	11	100.0	110	AJ709561	AJ709561 AJ709561
13	11	100.0	112	CG626392	OST334302
14	11	100.0	113	CV327048	CM4-UT004
15	11	100.0	113	BH367369	AG-ND-142
16	11	100.0	114	AA703431	z113a08.s
17	11	100.0	114	AZ537048	AST-2P014
18	11	100.0	115	BF988196	PW2-GN001
19	11	100.0	116	BF840511	RC6-HT100
20	11	100.0	119	BZ752975	PUPFA76TD
21	11	100.0	121	BM481440	533678 MA
22	11	100.0	123	CD267768	tab10b04
23	11	100.0	123	CV349851	MR2-NT013
24	11	100.0	130	BG315020	OP3-0.115

C 25	11	100.0	130	9	CL693344	CL693344 PRI0161b
26	11	100.0	131	2	AW837764	CM1-LT004
C 27	11	100.0	133	1	AA426670	AA426670 TEUF0193
28	11	100.0	134	8	EZ642070	EZ642070 OGANC58TM
29	11	100.0	135	7	CN561395	CN561395 tag68a11
30	11	100.0	135	8	CC178808	CC178808 XB063 Bay
C 31	11	100.0	136	8	AZ664763	AZ664763 LM0545A19
C 32	11	100.0	139	1	AA095286	AA095286 12132.8eq
33	11	100.0	139	2	BF739127	BF739127 FM2-KT000
34	11	100.0	139	8	EZ274920	EZ274920 CH230-355
35	11	100.0	140	9	CG732105	CG732105 1119146B1
C 36	11	100.0	142	2	BF935318	BF935318 CM1-NT027
C 37	11	100.0	145	4	BI133732	BI133732 UI-M-BH3
C 38	11	100.0	148	5	BP094741	BP094741 BP094741
C 39	11	100.0	149	2	BF092197	BF092197 RCO-TN008
40	11	100.0	150	8	CC065392	CC065392 fgma004f0
41	11	100.0	150	9	AG269438	AG269438 Cyanidlos
42	11	100.0	151	1	AV041964	AV041964 AV041964
43	11	100.0	153	2	BF172673	BF172673 PCL5476 M
44	11	100.0	154	8	B62266	B62266 T21A18TF TA
C 45	11	100.0	155	7	CK192778	CK192778 EST782093

ALIGNMENTS

RESULT 1
CN869358
LOCUS
DEFINITION
001202AAO06226HT (AAOA) Royal Gala phloem Malus x domestica CDNA
clone AAOA006226, mRNA sequence.
67 bp mRNA linear EST 03-JUN-2004
CN869358
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Malus x domestica (cultivated apple)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 67)
REFERENCE
AUTHORS
McAtney, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McAtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
CONTACT: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers
1. 67
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAOA006226"
/tissue_type="Phloem, scrapings from inside of bark mature wood"
/clone_lib="(AAOA) Royal Gala phloem"
/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

FEATURES
source

ORIGIN

Query Match 100.0%; Score 11; DB 7; Length 67;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGTGTACAGC 11
Db 43 GTGTGTACAGC 53

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 61.867 Seconds
(without alignments)
1103.355 Million cell updates/sec

Title: US-09-943-115A-15

Perfect score: 11

Sequence: 1 gtgtgtacagc 11

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	10	US-09-943-115A-15
2	11	100.0	11	10	Sequence 15, Appl
3	11	100.0	25	21	US-09-943-115A-16
4	11	100.0	25	21	Sequence 16, Appl
5	11	100.0	25	21	Sequence 13901, A
6	11	100.0	25	21	Sequence 13901, A
7	11	100.0	25	21	Sequence 13901, A
8	11	100.0	25	21	Sequence 13901, A
9	11	100.0	25	21	Sequence 13901, A
10	11	100.0	25	21	Sequence 13901, A
11	11	100.0	25	21	Sequence 13901, A
12	11	100.0	25	21	Sequence 13901, A
13	11	100.0	25	21	Sequence 13901, A
14	11	100.0	25	21	Sequence 13901, A
15	11	100.0	25	21	Sequence 13901, A
16	11	100.0	25	21	Sequence 13901, A
17	11	100.0	25	21	Sequence 13901, A
18	11	100.0	25	21	Sequence 13901, A
19	11	100.0	25	21	Sequence 13901, A
20	11	100.0	25	21	Sequence 13901, A
21	11	100.0	25	21	Sequence 13901, A
22	11	100.0	25	21	Sequence 13901, A
23	11	100.0	25	21	Sequence 13901, A
24	11	100.0	25	21	Sequence 13901, A
25	11	100.0	25	21	Sequence 13901, A
26	11	100.0	25	21	Sequence 13901, A
27	11	100.0	25	21	Sequence 13901, A
28	11	100.0	25	21	Sequence 13901, A
29	11	100.0	25	21	Sequence 13901, A
30	11	100.0	25	21	Sequence 13901, A
31	11	100.0	25	21	Sequence 13901, A
32	11	100.0	25	21	Sequence 13901, A
33	11	100.0	25	21	Sequence 13901, A
34	11	100.0	25	21	Sequence 13901, A
35	11	100.0	25	21	Sequence 13901, A
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C 8	11	100.0	25	21	US-10-719-900-439658
C 9	11	100.0	25	21	US-10-719-900-539744
C 10	11	100.0	25	21	US-10-719-900-552782
C 11	11	100.0	25	21	US-10-719-900-573524
C 12	11	100.0	25	21	US-10-719-900-573525
C 13	11	100.0	25	21	US-10-719-900-573525
C 14	11	100.0	25	21	US-10-719-900-573525
C 15	11	100.0	25	21	US-10-719-900-709974
C 16	11	100.0	25	21	US-10-719-900-741261
C 17	11	100.0	25	21	US-10-719-900-765849
C 18	11	100.0	25	21	US-10-719-900-789331
C 19	11	100.0	25	21	US-10-719-900-838664
C 20	11	100.0	25	21	US-10-719-900-838665
C 21	11	100.0	25	21	US-10-719-900-838665
C 22	11	100.0	25	21	US-10-809-189-29335
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C 24	11	100.0	25	21	US-10-809-189-29335
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C 29	11	100.0	25	21	US-10-809-189-29335
C 30	11	100.0	25	21	US-10-809-189-29335
C 31	11	100.0	25	21	US-10-809-189-29335
C 32	11	100.0	25	21	US-10-809-189-29335
C 33	11	100.0	25	21	US-10-809-189-29335
C 34	11	100.0	25	21	US-10-809-189-29335
C 35	11	100.0	25	21	US-10-809-189-29335
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C 45	11	100.0	25	21	US-10-809-189-29335

ALIGNMENTS

RESULT 1

US-09-943-115A-15

Sequence 15, Application US/09943115A

Publication No. US20030017469A1

GENERAL INFORMATION:

APPLICANT: SEQUENOM, Inc.

APPLICANT: Risinger, Carl

APPLICANT: Andersson, Maria

APPLICANT: Lewander, Tommy

APPLICANT: Olaiasson, Erik

TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9

FILE REFERENCE: POLYMORPHISMS

FILE REFERENCE: 52459-20021.00

CURRENT APPLICATION NUMBER: US/09/943,115A

PRIOR FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: UK 0021286.0

PRIOR FILING DATE: 2000-08-30

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15

LENGTH: 11

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide of the novel polymorphic site 461

OTHER INFORMATION: on the coding strand

US-09-943-115A-15

Query Match 100.0%; Score 11; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 19, 2005, 15:12:33 ; Search time 10.9221 Seconds
(without alignments)
5961.965 Million cell updates/sec

Title: US-09-943-115A-15
Perfect score: 11
Sequence: 1 gtgtgtacagc 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
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8: Geneseq2003as:*
9: Geneseq2003bs:*
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11: Geneseq2003ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	11	6	ABK68760 Oligonucl
C 2	11	100.0	11	6	ABK68759 Oligonucl
C 3	11	100.0	50	6	ABZ00444 Human leu
C 4	11	100.0	65	6	ABN32099 Rat splc
C 5	11	100.0	83	3	AAC08885 Human sec
C 6	11	100.0	137	3	AA43131 Human sec
C 7	11	100.0	154	4	AA149406 Probe #18
C 8	11	100.0	155	2	AAH85562 Human sin
C 9	11	100.0	155	2	AAH85561 Human sin
C 10	11	100.0	168	3	AAC30295 Human sec
C 11	11	100.0	169	3	AAA48201 Intron 4
C 12	11	100.0	195	12	ACH82368 Human gen
C 13	11	100.0	201	12	ADM97390 Prostate
C 14	11	100.0	201	12	ADM97385 Prostate
C 15	11	100.0	202	3	AAC31408 Human sec
C 16	11	100.0	233	3	AAC06071 Human sec
C 17	11	100.0	245	2	AAQ76753 Human sec
C 18	11	100.0	250	5	ABV48999 Human pro
C 19	11	100.0	252	2	AAQ60885 Human bra
C 20	11	100.0	252	8	ABX39550 Bovine ES

C 21	11	100.0	257	4	AAS24522 Human ova
C 22	11	100.0	259	8	ABZ19547 Group III
C 23	11	100.0	259	8	ABZ19167 Group III
C 24	11	100.0	259	8	ABZ19345 Group III
C 25	11	100.0	260	12	ACH83323 Human gen
C 26	11	100.0	261	12	ADJ25701 DNA encod
C 27	11	100.0	269	5	AAS81552 DNA encod
C 28	11	100.0	291	3	AAC24490 Human sec
C 29	11	100.0	292	6	ABN96731 Gene #322
C 30	11	100.0	305	5	AAS79399 DNA encod
C 31	11	100.0	305	13	ADR13241 Human can
C 32	11	100.0	309	5	AAH81601 Human dif
C 33	11	100.0	331	9	ACH28094 Human adu
C 34	11	100.0	332	9	ACH24679 Human adu
C 35	11	100.0	334	3	AAC16060 Human sec
C 36	11	100.0	340	4	AAK78102 Human imm
C 37	11	100.0	340	4	AAK78104 Human sec
C 38	11	100.0	340	8	ADA41626 Human sec
C 39	11	100.0	340	8	ADA41627 Human sec
C 40	11	100.0	340	10	ADA57762 BAC fragm
C 41	11	100.0	340	10	ADA57763 BAC fragm
C 42	11	100.0	362	13	ADQ51775 Novel can
C 43	11	100.0	365	5	AAH83130 Human ova
C 44	11	100.0	367	2	AAV86729 EST clone
C 45	11	100.0	377	11	ADP65928 Mouse EST

ALIGNMENTS

RESULT 1

ABK68760/c

ID ABK68760 standard; DNA; 11 BP.

XX

AC ABK68760;

XX

DT 02-JUL-2002 (first entry)

XX

DE Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.

XX

KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;

XX

OS Homo sapiens.

XX

FN WO200218641-A2.

XX

PD 07-MAR-2002.

XX

PF 30-AUG-2001; 2001WO-18001580.

XX

PR 30-AUG-2000; 2000GB-00021286.

XX

PA (GEMI-) GEMINI GENOMICS PLC.

XX

PI Risinger C, Andersson MK, Lewander T, Olaiasson E;

XX

DR WPI; 2002-351712/38.

XX

PT Novel primer pairs and sequence determination oligonucleotides useful for

XX

PT amplifying and detecting novel single nucleotide polymorphisms in the 5'

XX

PT flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes

XX

PS Claim 4; Page 17; 47pp; English.

XX

CC The present invention relates to PCR primer pairs for amplifying and

CC sequence determination oligonucleotides for detecting single nucleotide

CC polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450

CC (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position

CC 461 of a defined 1345 base pair sequence for CYP3A4 or position 957,

CC 1049, 1164, 1536, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.

CC The PCR primers are useful for amplifying the CYP sequences and the

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 19:46:29 ; Search time 3.1551 Seconds
(without alignments)
5704.747 Million cell updates/sec

Title: US-09-943-115A-15
Perfect score: 11
Sequence: 1 GTGTGTACAGC 11

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfileseq1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	25	4	US-09-396-196G-29335
2	11	100.0	25	4	US-09-396-196G-69385
3	11	100.0	83	4	US-09-513-999C-12960
4	11	100.0	146	1	US-08-062-472B-33
5	11	100.0	168	4	US-09-513-999C-34370
6	11	100.0	202	4	US-09-513-999C-35483
7	11	100.0	221	4	US-09-270-767-6886
8	11	100.0	221	4	US-09-270-767-22168
9	11	100.0	233	4	US-09-513-999C-10146
10	11	100.0	291	4	US-09-513-999C-28565
11	11	100.0	334	4	US-09-513-999C-20135
12	11	100.0	370	4	US-09-621-976-9081
13	11	100.0	430	4	US-09-513-999C-413
14	11	100.0	438	4	US-09-949-016-916
15	11	100.0	438	4	US-09-949-016-4050
16	11	100.0	443	3	US-08-903-139B-17
17	11	100.0	447	4	US-09-270-767-5014
18	11	100.0	447	4	US-09-270-767-20296
19	11	100.0	480	4	US-09-710-279-763
20	11	100.0	482	4	US-09-513-999C-3947
21	11	100.0	490	3	US-09-349-884-3
22	11	100.0	517	4	US-09-270-767-3142
23	11	100.0	517	4	US-09-270-767-18424
24	11	100.0	517	4	US-09-854-133-671
25	11	100.0	518	4	US-09-621-976-3448
26	11	100.0	595	3	US-09-740-235-6
27	11	100.0	601	4	US-09-949-016-18083

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28 11 100.0 601 4 US-09-949-016-22957 Sequence 22957, A
29 11 100.0 601 4 US-09-949-016-24858 Sequence 24858, A
30 11 100.0 601 4 US-09-949-016-24859 Sequence 24859, A
31 11 100.0 601 4 US-09-949-016-25315 Sequence 25315, A
32 11 100.0 601 4 US-09-949-016-25316 Sequence 25316, A
33 11 100.0 601 4 US-09-949-016-26337 Sequence 26337, A
34 11 100.0 601 4 US-09-949-016-26332 Sequence 26332, A
35 11 100.0 601 4 US-09-949-016-29322 Sequence 29322, A
36 11 100.0 601 4 US-09-949-016-30005 Sequence 30005, A
37 11 100.0 601 4 US-09-949-016-35609 Sequence 35609, A
38 11 100.0 601 4 US-09-949-016-35610 Sequence 35610, A
39 11 100.0 601 4 US-09-949-016-35611 Sequence 35611, A
40 11 100.0 601 4 US-09-949-016-56230 Sequence 56230, A
41 11 100.0 601 4 US-09-949-016-63015 Sequence 63015, A
42 11 100.0 601 4 US-09-949-016-65812 Sequence 65812, A
43 11 100.0 601 4 US-09-949-016-71259 Sequence 71259, A
44 11 100.0 601 4 US-09-949-016-71260 Sequence 71260, A
45 11 100.0 601 4 US-09-949-016-71261 Sequence 71261, A

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ALIGNMENTS

RESULT 1
US-09-396-196G-29335
; Sequence 29335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-29335

Query Match: 100.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTGTGTACAGC 11
Db 9 GTGTGTACAGC 19

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RESULT 2
US-09-396-196G-69385/c
; Sequence 69385, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69385

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 96.5227 Seconds
(without alignments)
4337.914 Million cell updates/sec

Title: US-09-943-115A-16

Perfect score: 11

Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY_NUC

Gap 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST:

1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 3	11	100.0	70	8	AZ875009
C 4	11	100.0	71	8	AZ936554
C 5	11	100.0	85	9	CR181730
C 6	11	100.0	93	7	CR440674
C 7	11	100.0	100	6	CB395011
C 8	11	100.0	103	7	CV364386
C 9	11	100.0	104	4	B1017585
C 10	11	100.0	106	9	CR058606
C 11	11	100.0	108	2	BF334323
C 12	11	100.0	110	1	AJ709561
C 13	11	100.0	112	9	CG626392
C 14	11	100.0	113	7	CV327048
C 15	11	100.0	113	8	BH367369
C 16	11	100.0	114	1	AA703431
C 17	11	100.0	114	8	AZ537048
C 18	11	100.0	115	4	BF988196
C 19	11	100.0	116	2	BF840511
C 20	11	100.0	119	8	BZ752975
C 21	11	100.0	121	4	BM481440
C 22	11	100.0	123	6	CD267768
C 23	11	100.0	123	7	CV349851
C 24	11	100.0	130	4	BG315020

25 11 100.0 130 9 CL693344
c 26 11 100.0 131 2 AW837764
27 11 100.0 133 1 AA426670
c 28 11 100.0 134 8 BZ642070
c 29 11 100.0 135 7 CN561395
c 30 11 100.0 135 8 CC178808
31 11 100.0 136 8 AZ664763
32 11 100.0 139 1 AA095286
c 33 11 100.0 139 2 BF739127
c 34 11 100.0 139 8 BZ274920
c 35 11 100.0 140 9 CG732105
36 11 100.0 142 2 BF935318
37 11 100.0 145 4 B1133732
38 11 100.0 148 5 BP094741
39 11 100.0 149 2 BF092197
c 40 11 100.0 150 8 CC065392
c 41 11 100.0 150 9 AG269438
c 42 11 100.0 151 1 AV041964
c 43 11 100.0 153 2 BF172673
c 44 11 100.0 154 8 B62266
c 45 11 100.0 155 7 CK192778

ALIGNMENTS

RESULT 1
CN869358/67 bp mRNA linear EST 03-JUN-2004
LOCUS 001202AAOA006226HT (AAOA) Royal Gala phloem Malus x domestica cDNA
DEFINITION clone AAOA006226, mRNA sequence.
ACCESSION CN869358
VERSION CN869358.1 GI:48126987
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
REFERENCE
AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
TITLE HortResearch Apple EST-Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers
1. .67
/organism="Malus x domestica"
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/clone_lib=" (AAOA) Royal Gala phloem"
/notes="Vector: pBluescript SK(-); Library sequenced by Genesis Research & Development"

FEATURES

source
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ORIGIN

Query Match 100.0%; Score 11; DB 7; Length 67;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGTACACAC 11
Db 53 GCTGTACACAC 43

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 61.8867 Seconds
(without alignments)
1103.355 Million cell updates/sec

Title: US-09-943-115A-16
Perfect score: 11
Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues
Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
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22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	11	10	US-09-943-115A-15
C 2	11	100.0	11	10	US-09-943-115A-16
C 3	11	100.0	25	21	US-10-719-900-13901
C 4	11	100.0	25	21	US-10-719-900-69725
C 5	11	100.0	25	21	US-10-719-900-136326
C 6	11	100.0	25	21	US-10-719-900-157636
C 7	11	100.0	25	21	US-10-719-900-273308

Sequence 438658,
Sequence 539744,
Sequence 552782,
Sequence 573524,
Sequence 573525,
Sequence 638285,
Sequence 709974,
Sequence 741261,
Sequence 765849,
Sequence 789331,
Sequence 838664,
Sequence 838665,
Sequence 976687,
Sequence 29335, A
Sequence 69385, A
Sequence 233704,
Sequence 435, App
Sequence 4847, Ap
Sequence 3917, Ap
Sequence 5639, Ap
Sequence 1793, Ap
Sequence 32776, A
Sequence 19639, A
Sequence 19294, A
Sequence 2012, Ap
Sequence 21601, A
Sequence 15563, A
Sequence 11490, A
Sequence 11492, A
Sequence 12160, A
Sequence 24597, A
Sequence 29823, A
Sequence 66110, A
Sequence 9514, Ap
Sequence 14106, A
Sequence 86457, A
Sequence 1144, Ap
Sequence 58061, A

ALIGNMENTS

RESULT 1
US-09-943-115A-15/c
; Publication 15, Application US/09943115A
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943.115A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide of the novel polymorphic site 461
; OTHER INFORMATION: on the coding strand
US-09-943-115A-15

Query Match 100.0% Score 11; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 19:46:29 ; Search time 3.1551 Seconds
(without alignments)
5704.747 Million cell updates/sec

Title: US-09-943-115A-16

Perfect score: 11

Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A-COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B-COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A-COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B-COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCTUS-COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	25	4	US-09-396-196G-29335
C 2	11	100.0	25	4	US-09-396-196G-69385
C 3	11	100.0	83	4	US-09-513-999C-12960
C 4	11	100.0	146	1	US-08-062-4728-33
C 5	11	100.0	168	4	US-09-513-999C-34370
C 6	11	100.0	202	4	US-09-513-999C-35483
C 7	11	100.0	221	4	US-09-270-767-6886
C 8	11	100.0	221	4	US-09-270-767-22168
C 9	11	100.0	233	4	US-09-513-999C-10146
C 10	11	100.0	291	4	US-09-513-999C-28565
C 11	11	100.0	334	4	US-09-513-999C-20135
C 12	11	100.0	370	4	US-09-621-976-9081
C 13	11	100.0	430	4	US-09-513-999C-413
C 14	11	100.0	438	4	US-09-949-016-916
C 15	11	100.0	438	4	US-09-949-016-4050
C 16	11	100.0	443	3	US-08-903-1398-17
C 17	11	100.0	447	4	US-09-270-767-5014
C 18	11	100.0	447	4	US-09-270-767-20296
C 19	11	100.0	480	4	US-09-710-279-763
C 20	11	100.0	482	4	US-09-513-999C-3947
C 21	11	100.0	490	3	US-09-349-884-3
C 22	11	100.0	517	4	US-09-270-767-3142
C 23	11	100.0	517	4	US-09-270-767-18424
C 24	11	100.0	517	4	US-09-854-133-671
C 25	11	100.0	518	4	US-09-621-976-3448
C 26	11	100.0	595	3	US-09-740-235-6
C 27	11	100.0	601	4	US-09-949-016-18083

C 28	11	100.0	601	4	US-09-949-016-22957	Sequence 22957, A
C 29	11	100.0	601	4	US-09-949-016-24858	Sequence 24858, A
C 30	11	100.0	601	4	US-09-949-016-24859	Sequence 24859, A
C 31	11	100.0	601	4	US-09-949-016-25315	Sequence 25315, A
C 32	11	100.0	601	4	US-09-949-016-25316	Sequence 25316, A
C 33	11	100.0	601	4	US-09-949-016-26336	Sequence 26336, A
C 34	11	100.0	601	4	US-09-949-016-26337	Sequence 26337, A
C 35	11	100.0	601	4	US-09-949-016-29322	Sequence 29322, A
C 36	11	100.0	601	4	US-09-949-016-30005	Sequence 30005, A
C 37	11	100.0	601	4	US-09-949-016-35609	Sequence 35609, A
C 38	11	100.0	601	4	US-09-949-016-35610	Sequence 35610, A
C 39	11	100.0	601	4	US-09-949-016-35611	Sequence 35611, A
C 40	11	100.0	601	4	US-09-949-016-36230	Sequence 36230, A
C 41	11	100.0	601	4	US-09-949-016-63015	Sequence 63015, A
C 42	11	100.0	601	4	US-09-949-016-65812	Sequence 65812, A
C 43	11	100.0	601	4	US-09-949-016-71259	Sequence 71259, A
C 44	11	100.0	601	4	US-09-949-016-71260	Sequence 71260, A
C 45	11	100.0	601	4	US-09-949-016-71261	Sequence 71261, A

ALIGNMENTS

RESULT 1
US-09-396-196G-29335/c
; Sequence 29335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-29335

Query Match 100.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTGTACACAC 11
Db 19 GCTGTACACAC 9

RESULT 2
US-09-396-196G-69385
; Sequence 69385, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69385

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OM nucleic - nucleic search, using sw model
Run on: June 19, 2005, 15:12:33 ; Search time 10.9221 Seconds
(without alignments)
5961.965 Million cell updates/sec

Title: US-09-943-115A-16
Perfect score: 11
Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001s:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2002bs:*
8: Geneseqn2003s:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	6	ABK68760
2	11	100.0	11	6	ABK68759
3	11	100.0	50	6	ABZ00444
4	11	100.0	65	6	ABN32099
5	11	100.0	83	3	AAO08885
6	11	100.0	137	3	AAA43131
7	11	100.0	154	4	AAI49406
8	11	100.0	155	2	AAH85562
9	11	100.0	155	2	AAH85561
10	11	100.0	168	3	AAO30295
11	11	100.0	169	3	AAA48201
12	11	100.0	195	12	ACH82368
13	11	100.0	201	12	ADM97390
14	11	100.0	201	12	ADM97385
15	11	100.0	202	3	AC311408
16	11	100.0	233	3	AAO6071
17	11	100.0	245	2	AAQ76753
18	11	100.0	250	5	ABV48999
19	11	100.0	252	2	AAQ60885
20	11	100.0	252	8	ABX39550

21	11	100.0	257	4	AAS24522
22	11	100.0	259	8	ABZ19547
23	11	100.0	259	8	ABZ19167
24	11	100.0	259	8	ABZ19345
25	11	100.0	260	12	ACH83323
26	11	100.0	261	12	ADJ25701
27	11	100.0	269	5	AAS81552
28	11	100.0	291	3	AAC24490
29	11	100.0	292	6	ABN96731
30	11	100.0	302	5	AAS79399
31	11	100.0	305	13	ADR13241
32	11	100.0	309	5	AAH81601
33	11	100.0	331	9	ACH28094
34	11	100.0	332	3	ACH24679
35	11	100.0	334	3	ACH16060
36	11	100.0	340	4	AAK78102
37	11	100.0	340	4	AAK78104
38	11	100.0	340	8	ADA41626
39	11	100.0	340	8	ADA41627
40	11	100.0	340	10	ADA57762
41	11	100.0	340	10	ADA57763
42	11	100.0	362	13	ADQ51775
43	11	100.0	365	5	AAH83130
44	11	100.0	367	2	AAV86729
45	11	100.0	377	11	ADP65928

ALIGNMENTS

RESULT 1
ABK68760
ID ABK68760 standard; DNA; 11 BP.
XX
AC ABK68760;
XX
02-JUL-2002 (first entry)
DE Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
XX
KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;
KW ss.
XX
OS Homo sapiens.
XX
FN WO200218641-A2.
XX
PD 07-MAR-2002.
XX
PF 30-AUG-2001; 2001WO-IB001580.
XX
PR 30-AUG-2000; 2000GB-00021286.
XX
XX (GEMI-) GEMINI GENOMICS PLC.
PI Risinger C, Andersson MK, Lewander T, Olafsson E;
XX
XX WPI; 2002-351712/38.
XX
XX Novel primer pairs and sequence determination oligonucleotides useful for
XX amplifying and detecting novel single nucleotide polymorphisms in the 5'
XX flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes
XX respectively.
XX
XX Claim 4; Page 17; 47pp; English.
XX
XX The present invention relates to PCR primer pairs for amplifying and
XX sequence determination oligonucleotides for detecting single nucleotide
XX polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450
XX (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position
XX 461 of a defined 1345 base pair sequence for CYP3A4 or position 957,
XX 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.
XX The PCR primers are useful for amplifying the CYP sequences and the

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:18:28 ; Search time 56.1997 Seconds
(without alignments)
9484.165 Million cell updates/sec

Title: US-09-943-115A-15

Perfect score: 11

Sequence: 1 gtgtgtacagc 11

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pa.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11	100.0	11	6	AX421267	AX421267 Sequence
2	11	100.0	11	6	AX421268	AX421268 Sequence
3	11	100.0	60	6	A29455	A29455 Sequence ex
4	11	100.0	61	9	HUMTCD1DG	L32456 Human (Clon
5	11	100.0	65	6	CQ535212	CQ535212 Sequence
6	11	100.0	83	6	AX897097	AX897097 Sequence
7	11	100.0	83	6	BD032630	BD032630 Sequence
8	11	100.0	110	11	AU048812	AU048812 Rattus no
9	11	100.0	123	11	AF235274	AF235274 Sus scro
10	11	100.0	133	4	AY434952	AY434952 Felis cat
11	11	100.0	146	6	I84526	I84526 Sequence 33
12	11	100.0	153	11	GI8652	GI8652 BMS1304 cow
13	11	100.0	154	6	CQ109233	CQ109233 Sequence
14	11	100.0	163	11	BV101004	BV101004 RPAMSE00
15	11	100.0	168	6	AX918507	AX918507 Sequence
16	11	100.0	168	6	BD054040	BD054040 Sequence
17	11	100.0	169	9	HSU52166	U52166 Human tumor
18	11	100.0	188	5	AB010782	AB010782 Hexagramm
19	11	100.0	194	11	AF253624	AF253624 Sus scro

20	11	100.0	201	11	BV205410	BV205410 sqm21813
21	11	100.0	202	6	AX919620	AX919620 Sequence
22	11	100.0	202	6	BD055153	BD055153 Sequence
23	11	100.0	204	6	CQ748128	CQ748128 Sequence
24	11	100.0	221	6	AR501926	AR501926 Sequence
25	11	100.0	221	6	AR517208	AR517208 Sequence
26	11	100.0	233	6	AX894283	AX894283 Sequence
27	11	100.0	233	6	BD029816	BD029816 Sequence
28	11	100.0	235	5	AF330225	AF330225 Oncorhyn
29	11	100.0	238	5	CR390323	CR390323 Gallus ga
30	11	100.0	244	5	SSA402851	AJ402851 Salmo sal
31	11	100.0	245	6	A74667	A74667 Sequence 35
32	11	100.0	245	6	A77646	A77646 Sequence 35
33	11	100.0	248	9	HS265VB1	Z23877 H. sapiens
34	11	100.0	248	11	AF013210	AF013210 Rattus no
35	11	100.0	250	6	CQ517151	CQ517151 Sequence
36	11	100.0	256	11	AU026314	AU026314 Rattus no
37	11	100.0	257	6	AX208863	AX208863 Sequence
38	11	100.0	261	6	CQ765925	CQ765925 Sequence
39	11	100.0	265	11	G25356	G25356 human STS E
40	11	100.0	273	11	AU028591	AU028591 Rattus no
41	11	100.0	279	5	HCH388044	AJ388044 Hyla chry
42	11	100.0	281	6	CQ703253	CQ703253 Sequence
43	11	100.0	287	11	G64262	G64262 AMHR2/ex11
44	11	100.0	291	6	AX912702	AX912702 Sequence
45	11	100.0	291	6	BD048235	BD048235 Sequence

ALIGNMENTS

RESULT 1	AX421267	11 bp	DNA	linear	PAT 18-JUN-2002
LOCUS	Sequence 15 from Patent WO0218641.				
DEFINITION	AX421267				
ACCESSION	AX421267.1				
VERSION	AX421267.1	GI:21524675			
KEYWORDS	synthetic construct				
SOURCE	other sequences; artificial sequences.				
ORGANISM	1				
REFERENCE	Risinger, C., Anderson, M.K., Lewander, T. and Olafsson, E.				
AUTHORS	Detection of cyp3a4 and cyp2c9 polymorphisms				
TITLE	Patent: WO 0218641-A 15 07-MAR-2002;				
JOURNAL	Gemini Genomics PLC (GB)				
FEATURES	Location/Qualifiers				
source	1..11				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Oligonucleotide of the novel polymorphic site 461 on the coding strand"				

ORIGIN

Query Match	100.0%;	Score 11;	DB 6;	Length 11;
Best Local Similarity	100.0%;	Pred. No. 7.3e+04;		
Matches	11;	Conservative	0;	Mismatches 0;
				Indels 0; Gaps 0;
Qy	1	GTGTGTACAGC 11		
Db	1	GTGTGTACAGC 11		
RESULT 2	AX421268/c			
LOCUS	AX421268	11 bp	DNA	linear
DEFINITION	Sequence 16 from Patent WO0218641.			
ACCESSION	AX421268			
VERSION	AX421268.1	GI:21524676		
KEYWORDS	synthetic construct			
SOURCE	1			
ORGANISM	1			

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:18:28 ; Search time 56.1997 Seconds
(without alignments)
9484.165 Million cell updates/sec

Title: US-09-943-115A-16
Perfect score: 11
Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	11	100.0	11	6	AX421267	AX421267 Sequence
C 2	11	100.0	11	6	AX421268	AX421268 Sequence
C 3	11	100.0	60	6	A29455	A29455 sequence ex
C 4	11	100.0	61	9	HOMTCVDLIG	L32456 Human (clon
C 5	11	100.0	65	6	CQ535212	CQ535212 Sequence
C 6	11	100.0	83	6	AX897097	AX897097 Sequence
C 7	11	100.0	83	6	BD032630	BD032630 Sequence
C 8	11	100.0	110	11	AU048812	AU048812 Rattus no
C 9	11	100.0	123	11	AF235274	.AF235274 Sus scrof
C 10	11	100.0	133	4	AY434952	AY434952 Felis cat
C 11	11	100.0	146	6	I84526	I84526 Sequence 33
C 12	11	100.0	153	11	G18652	G18652 BMS1304 cow
C 13	11	100.0	154	6	CQ109233	CQ109233 Sequence
C 14	11	100.0	163	11	BV101004	BV101004 RFAMWSEQO
C 15	11	100.0	168	6	AX918507	AX918507 Sequence
C 16	11	100.0	168	6	BD054040	BD054040 Sequence
C 17	11	100.0	169	9	H5U52166	US2166 Human tumor
C 18	11	100.0	188	5	AB010782	AB010782 Hexagramm
C 19	11	100.0	194	11	AF253624	AF253624 Sus scrof

C 20	11	100.0	201	11	BV205410	BV205410 sqnm21813
C 21	11	100.0	202	6	AX919620	AX919620 Sequence
C 22	11	100.0	202	6	BD055153	BD055153 Sequence
C 23	11	100.0	204	6	CQ748128	CQ748128 Sequence
C 24	11	100.0	221	6	AR501926	AR501926 Sequence
C 25	11	100.0	221	6	AR517208	AR517208 Sequence
C 26	11	100.0	233	6	AX894283	AX894283 Sequence
C 27	11	100.0	233	6	BD029816	BD029816 Sequence
C 28	11	100.0	235	5	AF330225	AF330225 Oncorhync
C 29	11	100.0	238	5	CR390323	CR390323 Gallus ga
C 30	11	100.0	244	5	SSA402851	AJ402851 Salmo sal
C 31	11	100.0	245	6	A74667	A74667 Sequence 35
C 32	11	100.0	245	6	A77646	A77646 Sequence 35
C 33	11	100.0	248	9	HS265VB1	Z23877 H. sapiens
C 34	11	100.0	248	11	AF013210	AU113210 Rattus no
C 35	11	100.0	250	6	CQ517151	CQ517151 Sequence
C 36	11	100.0	256	11	AU026314	AU026314 Rattus no
C 37	11	100.0	257	6	AX208863	AX208863 Sequence
C 38	11	100.0	261	6	CQ765925	CQ765925 Sequence
C 39	11	100.0	265	11	G25356	G25356 human STS E
C 40	11	100.0	273	11	AU028591	AU028591 Rattus no
C 41	11	100.0	279	5	HCH388044	AJ388044 Hyla chry
C 42	11	100.0	281	6	CQ703253	CQ703253 Sequence
C 43	11	100.0	287	11	G64262	G64262 AMHR2/ex11
C 44	11	100.0	291	6	AX912702	AX912702 Sequence
C 45	11	100.0	291	6	BD048235	BD048235 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX421267 11 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 15 from Patent WO0218641.
ACCESSION AX421267
VERSION AX421267.1 GI:21524675
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Olaiasson,E.
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms
JOURNAL Patent: WO 0218641-A 15 07-MAR-2002;
GEMINI Genomics PLC (GB)
FEATURES
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1. .11
Location/Qualifiers
/organism="synthetic construct"
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/note="Oligonucleotide of the novel polymorphic site 461 on the coding strand"

Query Match 100.0%; Score 11; DB 6; Length 11;
Best local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGTACACAC 11
DB 11 GCTGTACACAC 1

ORIGIN

AX421268
LOCUS AX421268 11 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 16 from Patent WO0218641.
ACCESSION AX421268
VERSION AX421268.1 GI:21524676
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 11802.1 Seconds
(without alignments)
4337.914 Million cell updates/sec

Title: US-09-943-115A-1
Perfect score: 1345
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	186.6	13.9	872	CR810224	GR0AAA33C
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8	164	12.2	582	BP270391	BP270391
9	163.6	12.2	599	BP383396	BP383396
10	162.4	12.1	650	AV654562	AV654562
11	160.6	11.9	358	AV660310	AV660310
12	156.4	11.6	364	AV655529	AV655529
13	153.6	11.4	584	AV657970	AV657970
14	152	11.3	298	CR788987	DKF2p469L
15	151	11.2	755	EX643367	EX643367
16	150.8	11.2	771	AV646975	AV646975
17	147.8	11.0	411	TV1511	TV1511
18	144.6	10.8	262	TV4622	YC57a05.r1
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20	143	10.6	934	CO581493	ILLUMINIGEN
21	142.2	10.5	821	CO582079	ILLUMINIGEN
22	141	10.5	165	AU076847	AU076847
23	140	10.4	875	EX445330	EX445330
24	140	10.4	1090	EX428031	EX428031

25	139.8	10.4	870	7	CO583597	CO583597
26	139.8	10.4	943	7	CO583293	ILLUMINIGEN
27	138.8	10.4	982	7	CO581624	ILLUMINIGEN
28	139.6	10.4	947	5	EX388061	EX388061
29	139.2	10.3	938	5	EX422263	EX422263
30	139	10.3	314	7	T68354	YC41C05.r1
31	137.4	10.2	380	5	EX494898	DKF2p779E
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33	137	10.2	922	5	EX463042	EX463042
34	137	10.2	942	1	AL531737	AL531737
35	136	10.1	734	7	CF271965	AGENCOURT
36	136	10.1	748	7	CF271966	AGENCOURT
37	136	10.1	778	7	CK130234	AGENCOURT
38	136	10.1	779	7	CF271964	AGENCOURT
39	136	10.1	780	7	CK130233	AGENCOURT
40	135.8	10.1	841	5	EX449069	EX449069
41	135.2	10.1	681	5	EX951468	DKF2p781D
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ALIGNMENTS

RESULT 1
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LOCUS HSC 00196 RPCI-11 Human Male BAC Library Homo sapiens genomic clone
DEFINITION HSC 00196 RPCI-11 Human Male BAC Library Homo sapiens genomic clone
ACCESSION AZ537700
VERSION AZ537700.1 GI:11125732
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 606)
AUTHORS Scherer, S.W., Rommens, J.M. and Tsui, L.C.
TITLE Gene Identification on Human Chromosome 7
JOURNAL Unpublished (2000)
COMMENT Contact: Scherer, S.W.; Rommens, J.M.; Tsui, L.C.; Boright, A.P.
The Human Chromosome 7 Project
Department of Genetics, The Hospital for Sick Children
555 University Avenue, Toronto, Ontario M5G 1X8, Canada
Tel: 416 813 7613
Fax: 416 813 8319
Email: steve@genet.sickkids.on.ca
Clone maps to Yq22 (contains CYP3A5, CYP3A7, D7S2432, D7S647,
D7S1678, D7S2832)
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 606.
Location/Qualifiers
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/clone="H NH0513J13"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/notes="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

FEATURES
source
1. 606
Location/Qualifiers

ORIGIN

Query Match 30.7%; Score 413; DB 8; Length 606;
Best Local Similarity 89.2%; Pred. No. 2.3e-108;
Matches 502; Conservative 1; Mismatches 45; Indels 15; Gaps 5;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 7567.05 Seconds
(without alignments)
1103.355 Million cell updates/sec

Title: US-09-943-115A-1

Perfect score: 1345

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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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SUMMARIES

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4	1310	97.4	96960	21	US-10-484-577-662
5	1190.2	88.5	13035	15	US-10-121-960C-14
6	1153.2	85.7	15185	15	US-10-121-960C-17
7	1140.2	84.8	12983	21	US-10-415-607-1

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Sequence 4, Appli
Sequence 47, Appli
Sequence 48, Appli
Sequence 660, Appli
Sequence 149, Appli
Sequence 150, Appli
Sequence 662, Appli
Sequence 14, Appli
Sequence 297, Appli
Sequence 363, Appli
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Sequence 3816, Appli
Sequence 1405, Appli
Sequence 39, Appli
Sequence 40, Appli
Sequence 15077, Appli
Sequence 4176, Appli
Sequence 6070, Appli
Sequence 8232, Appli
Sequence 9871, Appli
Sequence 3467, Appli

8 924.4 68.7 11186 9 US-09-957-997-1
9 924.4 68.7 11186 21 US-10-415-607-4
10 813.2 60.5 1012 9 US-09-957-997-4
11 646.4 48.1 8943 17 US-10-257-166-47
12 578.8 43.0 8943 17 US-10-257-166-48
13 518.4 38.5 177531 21 US-10-484-577-660
14 496.8 36.9 1254 14 US-10-085-612-4
15 309.6 23.0 8776 17 US-10-257-166-149
16 237.4 17.7 8776 17 US-10-257-166-150
17 227.4 16.9 96960 21 US-10-484-577-662
18 177.6 13.2 2768 16 US-10-268-822-14
19 177.6 13.2 2768 17 US-10-388-360-237
20 177.6 13.2 2768 17 US-10-388-360-237
21 163.6 12.2 2059 18 US-10-641-643-1062
22 136 10.1 1595 15 US-10-106-698-1724
23 135.6 10.1 2759 14 US-10-146-575-1
24 135.2 10.1 2849 9 US-09-880-107-2110
25 123 9.1 2011 9 US-09-880-107-1586
26 119 8.8 1707 9 US-09-880-107-2114
27 119 8.8 1707 18 US-10-641-643-1060
28 118 8.8 384 9 US-09-925-297-24
29 115.8 8.6 1659 13 US-10-007-814-1
30 113.4 8.4 1915 18 US-10-112-944-188
31 112 8.3 489 13 US-10-027-632-277590
32 112 8.3 489 17 US-10-027-632-277590
33 107.4 8.0 1525 9 US-09-880-107-3816
34 107.4 8.0 1599 18 US-10-641-643-1405
35 106 7.9 106 13 US-10-007-814-39
36 88.4 6.6 106 13 US-10-007-814-40
37 74.6 5.5 105 13 US-10-007-814-41
38 74.6 5.5 240 9 US-09-960-352-15077
39 74.6 5.5 380 9 US-09-960-352-15107
40 74.6 5.5 411 9 US-09-960-352-4176
41 74.6 5.5 422 9 US-09-960-352-6070
42 74.6 5.5 430 9 US-09-960-352-8232
43 73.6 5.5 1512 17 US-10-313-963A-55
44 73.2 5.4 207 9 US-09-960-352-9871
45 73.2 5.4 347 9 US-09-960-352-3467

ALIGNMENTS

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; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943.115A
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 99.9%; Score 1344.2; DB 10; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGAGTGACCACTGCGCCCATCTTGTGCTGAGGTGGGTGCTCATCTGGCTATCT 60

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 19:46:29 ; Search time 385.783 Seconds
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5704.747 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1344.2	99.9	1345	US-09-144-367-3	Sequence 3, Appl
4	1310	97.4	31197	US-09-949-016-12963	Sequence 12963, A
5	1310	97.4	103934	US-09-949-016-14433	Sequence 14433, A
6	1079.6	80.3	34172	US-09-949-016-14432	Sequence 14432, A
7	518.4	38.5	35803	US-09-949-016-11863	Sequence 11863, A
8	518.4	38.5	35804	US-09-949-016-12962	Sequence 12962, A
9	278.8	20.7	601	US-09-949-016-20240	Sequence 20240, A
10	278.8	20.7	601	US-09-949-016-42446	Sequence 42446, A
11	178.6	13.3	2079	US-09-949-016-2691	Sequence 2691, Ap
12	177.6	13.2	2768	US-09-949-016-1221	Sequence 1221, Ap
13	163.6	12.2	2059	US-09-023-655-1062	Sequence 1062, Ap
14	153.	11.4	2080	US-09-949-016-2690	Sequence 2690, Ap
15	135.6	10.1	2759	US-09-144-367-1	Sequence 1, Appl
16	124.4	9.2	601	US-09-949-016-93499	Sequence 93499, A
17	119	8.8	1707	US-09-023-655-1060	Sequence 1060, Ap
18	119	8.8	1707	US-09-949-016-121	Sequence 121, App
19	119	8.8	1707	US-09-949-016-1220	Sequence 1220, Ap
20	115.8	8.6	1659	US-09-583-447A-1	Sequence 1, Appl
21	107.4	8.0	1599	US-09-023-655-1405	Sequence 1405, Ap
22	106	7.9	106	US-09-583-447A-39	Sequence 39, Appl
23	88.4	6.6	106	US-09-583-447A-40	Sequence 40, Appl
24	74.6	5.5	105	US-09-583-447A-41	Sequence 41, Appl
25	73.6	5.5	1512	US-08-277-031B-4	Sequence 4, Appl
26	70	5.2	7218	US-08-232-463-14	Sequence 14, Appl
27	66	4.9	106	US-09-583-447A-42	Sequence 42, Appl

28 57 4.2 57 1 US-07-640-473-5 Sequence 5, Appl
29 57 4.2 57 1 PCT-US93-317-24 Sequence 24, Appl
30 57 4.2 57 5 PCT-US93-06171-24 Sequence 24, Appl
31 52.8 3.9 1192 4 US-09-583-447A-9 Sequence 9, Appl
32 52.8 3.9 1349 4 US-09-583-447A-5 Sequence 5, Appl
33 52.8 3.9 1515 4 US-09-583-447A-3 Sequence 3, Appl
34 52.8 3.9 1633 4 US-09-583-447A-7 Sequence 7, Appl
35 52.8 3.9 1973 4 US-09-583-447A-11 Sequence 11, Appl
36 49 3.6 57 1 US-07-640-473-13 Sequence 13, Appl
37 47.4 3.5 57 1 US-07-640-473-7 Sequence 7, Appl
38 47.4 3.5 57 1 US-07-640-473-11 Sequence 11, Appl
39 47.4 3.5 57 1 US-07-908-317-26 Sequence 26, Appl
40 47.4 3.5 57 5 PCT-US93-06171-26 Sequence 26, Appl
41 45.8 3.4 57 1 US-07-640-473-9 Sequence 9, Appl
42 43.4 3.2 243 3 US-09-172-108-12 Sequence 12, Appl
43 43.2 3.2 265 3 US-09-172-108-10 Sequence 10, Appl
44 40.6 3.0 601 4 US-09-949-016-162622 Sequence 162622,
45 40.6 3.0 140925 4 US-09-949-016-11777 Sequence 11777, A

ALIGNMENTS

RESULT 1

US-09-372-339-1
; Sequence 1, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebeck, Timothy
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-1

Query Match 99.9%; Score 1344.2; DB 3; Length 1345;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CTGCAGTGCACCACTGCCCCCATCATTTGCTGGCTGAGGTGGTGGGTCCATCTGGCTATCT 60
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GenCore version 5.1.6
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5961.965 Million cell updates/sec

Title: US-09-943-115A-1

Perfect score: 1345

Sequence: 1 ctgcagtgaccactgcccac.....cgtatcaggcctctctttt 1345

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1344.2	99.9	1345	2	AAX28296 Human CYP
2	1344.2	99.9	1345	3	AAX257019 Nucleic a
3	1344.2	99.9	1345	3	AAX257020 Nucleic a
4	1344.2	99.9	1345	6	ABK68745 5'-flanki
5	1344.2	99.9	1345	12	ADJ84441 Human phe
6	1310	97.4	6101	13	ADJ89077 Human CYP
7	1310	97.4	96960	8	ACF62734 Cancer ba
8	1310	97.4	96960	8	ADJ89077 Human CYP
9	1310	97.4	96960	10	ADJ89077 Human CYP
10	1310	97.4	96960	10	ADJ89077 Human CYP
11	1310	97.4	96960	10	ADJ89077 Human CYP
12	1310	97.4	96960	10	ADJ89077 Human CYP
13	1305.2	97.0	39071	12	ADJ89077 Human CYP
14	1190.2	88.5	13035	8	ADJ89077 Human CYP
15	1153.2	85.7	15185	8	ADJ89077 Human CYP
16	1140.2	84.8	12983	6	ADJ89077 Human CYP
17	924.4	68.7	11186	6	ADJ89077 Human CYP
18	924.4	68.7	11186	6	ADJ89077 Human CYP
19	817.6	60.8	6101	13	ADJ89077 Human CYP
20	814.4	60.6	6101	13	ADJ89077 Human CYP

21	813.2	60.5	1012	6	AAD36215	Aad36215 Human pro
22	746.8	55.5	6101	13	ADJ89077	Adj89077 Human CYP
23	743.6	55.3	6101	13	ADJ89077	Adj89077 Human CYP
24	646.4	48.1	8943	6	ABK39966	Abk39966 Human che
25	578.8	43.0	8943	6	ABK39966	Abk39966 Human che
26	518.4	38.5	36902	6	AAD43350	Aad43350 Human cyt
27	518.4	38.5	177531	8	ACF62732	Acf62732 Cancer ba
28	518.4	38.5	177531	8	ADJ89077	Adj89077 Human CYP
29	518.4	38.5	177531	10	ADJ89077	Adj89077 Human CYP
30	518.4	38.5	177531	10	ADJ89077	Adj89077 Human CYP
31	518.4	38.5	177531	10	ADJ89077	Adj89077 Human CYP
32	518.4	38.5	177531	10	ADJ89077	Adj89077 Human CYP
33	483.4	35.9	830	6	ABK99501	Abk99501 Human bac
34	481.8	35.8	830	6	ABK99501	Abk99501 Human bac
35	481.8	35.8	830	6	ABK99501	Abk99501 Human bac
36	481.8	35.8	830	6	ABK99501	Abk99501 Human bac
37	480.2	35.7	830	6	ABK99501	Abk99501 Human bac
38	480.2	35.7	830	6	ABK99501	Abk99501 Human bac
39	480.2	35.7	830	6	ABK99501	Abk99501 Human bac
40	480.2	35.7	830	6	ABK99501	Abk99501 Human bac
41	458.2	34.1	1001	13	ADQ81033	Adq81033 Human phe
42	438.4	32.6	1346	3	AAA51756	Aaa51756 Cytochrom
43	309.6	23.0	8776	6	ABK40067	Abk40067 Human che
44	291	21.6	1965	13	ACN41767	Acn41767 Human dia
45	291	21.6	2041	13	ACN41766	Acn41766 Human dia

ALIGNMENTS

RESULT 1

AAX28296
ID AAX28296 standard; DNA; 1345 BP.

XX AAX28296;

DT 17-JUN-1999 (first entry)

XX Human CYP3A4 gene promoter.

XX CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;
KW CYP3A4 substrate; drug-drug interaction identification; toxin exposure;
KW genetic linkage detection; phenotypic variation; promoter; ss.

XX Homo sapiens.

XX WO9913106-A1.

XX 18-MAR-1999.

XX 02-SEP-1998; 98WO-US018158.

XX 10-SEP-1997; 97US-0058612P.

XX (AAXS-) AAXS PHARM INC.

XX Lichter JB, Guida M;

XX WPI; 1999-215070/18.

XX New isolated CYP3A4 polymorphic sequences.

XX Disclosure; Page 29; 40pp; English.

XX This sequence represents the human CYP3A4 gene promoter. The invention relates to a CYP3A4 sequence polymorphism, which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYP3A4 polymorphic sequences can be used to screen patients for altered metabolism for CYP3A4 substrates, potential drug-drug interactions, and adverse/side effects as well as diseases that result from environmental or occupational exposure to toxins. They can also be used to establish animal, cell culture and in vitro cell-free models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used for expression studies to

